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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Sat May 13 08:01:01 2000; MasPar time 23.59 Seconds

Tabular output not generated.

Tabular output not generated.

Title: >US-09-331-631-1

Description: (1-666) from US09331631.pep (1 of 5)

Perfect Score: 4924

Sequence: 1 MAINTSNLCSLFLLSLFLL......SPRSTKQQQPLVSILDFVGF 666

Scoring table: PAM 150
Gap 11

188963 segs, 23686106 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Searched:

Database: a-geneseq35 1:geneseqp

Statistics: Mean 37.170; Variance 173.030; scale 0.215

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

22 23 23	10 11 13 13 14 15 16 17 18	13w4w01	Result.
146 143 137 139	964 930 924 917 883 883 155 155	4924 4746 4487 1330 1246 1178 1109 1063 1063	Score
NNN 8890	, 19.6 18.9 18.8 18.6 17.9 17.9 3.4 3.1	100.0 96.4 91.1 27.0 25.3 23.9 22.3 21.6	Query
1382 186 265 432	444 605 626 614 614 637 395 395	5 4 4 5 5 5 5 5 6 6 6 6 6 6 6 6 6 6 6 6	Length
			DB
W31867 W26536 R12844 W93954	W90340 W902838 W90342 W22150 W22149 W62834 W62837 W62837 W638474 R60054	W62828 W62829 W62830 R20181 R62832 W62832 W62833 W628331 W628331	Ħ
	G. max truncated SBP1 Glycine max antimicrob G. max truncated SBP2 Peanut allergen Ara hI Peanut allergen Ara hI Peanut allergen antimi Arachis hypogaea antimi Mouse SRY-related prot Dirofilaria immitis pa Polypeptide fragment e	Macadamia integrifolia Macadamia integrifolia Macadamia integrifolia Sequence encoded by 67 Gossypium hirsutum ant Theobroma cacao antimi Zea mays antimicrobial G. max SBP2 protein.	Description
3.34e-02 5.53e-02 1.50e-01 1.08e-01	6.98e-73 8.08e-70 2.80e-69 1.20e-68 1.37e-65 6.37e-65 6.40e-(.10) 7.22e-03 1.69e-02	0.00e+00 0.00e+00 0.00e+00 0.00e+00 4.68e-106 2.04e-98 3.05e-92 4.41e-82 7.99e-82 1.77e-78	Pred. No.
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24	137		541	_	W37148	Mammalian Ena (Mena). 1.50e-01
25	137	2! 8	783	\vdash	15	ral Mena+ pro 1.
8	137		787	٢	W37152	Mena++ pr 1
27	137	12.8	802	μ.	W37153	neural Mena+++ p 1
28	126	2.6	316	۳	R26941	LSA-R-NR 9
29	126	ນ໌ ດ	493	Н	R26944	LSA gene 9
30	121	2. 5	325	۳	W59645	equence of 2
31	122	2.5	351	Н	R24393	ie- 1
32	121	2.5	521	سر	W74802	٠
3	121	2.5	1178	۳	W30763	
34	123	2.5	1529	س	R97985	el 1
35	117	2.4	436	سر	W03662-	_
36	119	2.4	562	Н	R70491	Leucocytozoan protozoa 2.81e+00
37	117	2.4	614	μ	R82630	
38	113	بز د.	28	μ	W62841	Stenocarpus sinuatus a 7.22e+00
39	113	2.3	ω ω	Н	W62836	Zea mays antimicrobial 7.22e+00
40	114	2.3	314	Н	W88499	Human stomach carcinom 6.18e+00
41	112	2. 3	561	μ	P61363	Soybean glycinin A5A4B 8.44e+00
42	112	.2.3	918	\vdash	\sim	ecepto
43	112		919	Н	W14783	
44	112	•	919	سز	P93109	cepto
45	112	2.3	1343	سر	W31866	

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181	121	121	61	61	_	–	s 666; Conservative	Query Match 100.0%; Best Local Similarity 100.0%;	SQ Sequence 666 AA;	animals.	be used to control micro	The section of is that of	PT useful for controlling microbial infestations of			Bower NI, Goulter KC, WPI: 98-377279/32.	(RETR-) COOP RES CENT	20-DEC-1996;		PD 02-JUL-1998.	/note= "	Protein 29666	note= "	Peptide	Macadamia integr	antimicrobial protein;	Macadamia integrifolia		W62828 standard; Protein; 6	RESULT 1
	DPQQQYEQCQXHCQRRETEPRHWQTCQQRCERRYEKEKRKQQKRYEEQQREDEEKYEERA XFFFNAR DBQQLFYETO BBBCTTQQEBDQQQQT BCBBXQDDGKRYEEQQREDEEKYEERA	DPQQQYEQCQKHCQRRETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQQREDEEKYEERM	KRFEEDIDWSKYDNQEDPQTECQQCQRRCRQQESGPRQQQYCQRRCKEICEEEEEYNRQR	KRFEEDIDWSKYDNQEDPQTECQQCQRRCRQQESGPRQQQYCQRRCKEICEEEEEYNRQR	MAINTSNICSLIFLÄSLFLLSTTVSLAESEFDRQEYEECKRQCMQLETSGQMRRCVSQCD	MAINTSNLCSLLFLLSLFLLSTTVSLABSEFDRQEYEECKRQCMQLETSGQMRRCVSQCD	0;	Score 4924; DB 1; Length Pred. No. 0.00e+00;			nts and	£ 5.	plants			Green JL, Manners JM, Marcus JP;	TOHE				"mature protein"		"signal peptide"	128	One of the one	infestation; c	antimicrobial protein.	ry)	in; .666 AA.	
PORGESCRY 240	_	_	EEEEYNROR 120	EEEEEYNROR 120	MRRCVSQCD 60	OMRRCVSQCD 60	s 0; Gaps	666;			mammalian	2	or mammals	lfolia -																

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20-DEC-1996; AU-004275.
20-DEC-1996; AU-004275.
(RETR-) COOP RES CENT TROPICAL PL
BOWET NI, Goulter KC, Green JL, M
WPI, 98-377279/32.
N-PSDB; V42311.
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animals.
Sequence
                                                                                                                                                                                                                                                                                                                           Novel anti-microbial protein from e.g. Macadamia integruseful for controlling microbial infestations of plants Claim 1; Page 39-41; 96pp; English.
The sequence is that of an antimicrobial protein which be used to control microbial infestations in plants and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antimicrobial protein; infestation; c Macadamia integrifolia.
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W62829;
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                                         KRFEEDIDWSKYDNQDDDQTDCQQCQRRCRQQESGPRQQQYCQRRCKEICEEEEEYNRQR 120
                                                                                                                          MAINTSNICSLLFLLSLFLLSTTVSLAESEFDRQEYEECKRQCMQLETSGQMRRCVSQCD 60
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02-JUL-1998.

22-DEC-1997; AU0874.

20-DEC-1997; AU-004275.

(RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.

I Bower NI, Goulter KC, Green JL, Manners JM, Marcus R WPI; 98-377279/32.

R N-PSDB; V42316.

PT Novel anti-microbial protein from e.g. Macadamia useful for controlling microbial infestations of PS Claim 1; Page 43-45; 96pp: English.

CC The sequence is that of an antimicrobial protein has used to control microbial infestations in plants.
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Query Match
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Matches 60
                                    be used to control animals.
Sequence 625 AA;
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Macadamia integrifolia antimicrobial
antimicrobial protein; infestation;
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                                                                                                                                                                                         Protein
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          Similarity
$ 91.1%;
ilarity 96.6%;
Conservative
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                                                                                                                                                                               /note= "signal
29 666
/note= "mature
                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                           Protein;
Score 4487; DB 1;
Pred. No. 0.00e+00;
13; Mismatches 8;
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Recombliant Combined in large quantities.

beans and produced in large quantities.

expression vectors

Claim 4; Fig 2; 59pp; English.

The inventors claim a 67 kD and 31 kD T. cacao protein, and fragments, and encoding DNAs. The 47 kD and 31 kD proteins are derived from the 67 kD precursor. T. cacao protein cDNA was detected in a cDNA library prepared from immature cocoa beans RNA using a probe based on the AA sequence of a CNBr peptide common to the 47 kD and 31 kD polypeptides. Homology searches revealed close the 47 kD and 31 kD polypeptides and the vicilins, which are
                                                                                                                                                                                                                                                                                                                                                            11-JUN-1990; GB-013016.
(MRSC ) MARS UK LTD.
Spencer ME, Hodge R, Deakin
WPI; 92-024418/03.
                                                                                                                                                                                                                                                                                                                                       N-PSDB; Q20377
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11-JUN-1990;
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see encoded by 67 kD T. cacao protein cDNA.
flavour; vicilin; seed storage protein.
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animals.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                    antimicrobial protein;
Gossypium hirsutum.
WO9827805-Al.
                                                                                                                                                                             useful for controlling microbial infestations of plants or claim 1; Page 49-51; 96pp; English.
The sequence is that of an antimicrobial protein which can be used to control microbial infestations in plants and mar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W62832;
27-OCT-1998 (first entry)
Gossypium hirsutum antimic
                                                                                                                                                                                                                                                                              Novel anti-microbial protein from
                                                                                                                                                                                                                                                                                                          Bower NI, Goulter KC, WPI; 98-377279/32.
                                                                                                                                                                                                                                                                                                                                                     22-DEC-1997; AU0874.
20-DEC-1996; AU-004275.
(RETR-) COOP RES CENT 1
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Query Match Best Local

Matches

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Score 1246; DB 1; Pred. No. 2.04e-98; 150; Mismatches 144

144;

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Best Local S
Matches 19
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22-DEC-1997; AU0874.
20-DEC-1996; AU-004275.
20-DEC-1996; AU-004275.
(RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
RETR-) COULTER KC, Green JL, Manners JM, Mar Bower NI, Goulter KC, Green JL, Manners JM, Mar Bower NI, 98-377279/32.
                                                                                                                                                                                  Novel anti-microbial protein from e.g. Macadamia integriuseful for controlling microbial infestations of plants Claim 1; Page 47-49; 96pp; English.

The sequence is that of an antimicrobial protein which compared to control microbial infestations in plants and
                                                                                                                                                                                                                                                                                                                                                    Theobroma cacao antimicrobial protein. antimicrobial protein; infestation; co Theobroma cacao.
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W62831
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        QCQGRCQEQQQGQREQQQCQRKCWEQYKEQERGEHENYHNHK-KNRSEEEEEGQQRNNPYY 145
                                                                  ERDPRQQYEQCQRRCESE-ATEEREQE-QCE--QRCERE-YKEQQRQQEE--E-LQRQYQ 86
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|:| || | | :| : ||:|: |
VEESFNSQDQSIFFPGPRQHQQQS 647
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llarity 40.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                       Protein;
                                                                                                                                                                                                                           rotein from e.g. Macadamia integrifolia microbial infestations of plants or man
                                                                                                                                                                                                                                                                                                                                                                                                                        525
                                                                                                      Score 1178; DB 1;
Pred. No. 3.05e-92;
125; Mismatches 139;
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02-70TL-1998.

02-70TL-1998.

72-DEC-1997; AU0874.

72-DEC-1996; AU-004275.

R (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.

R (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.

R WPI, 988-377279/32.

R WPI, 988-377279/32.

T Novel anti-microbial protein from e.g. Macadamia integrife Novel anti-microbial protein infestations of plants or Claim 1; Page 58-60; 96pp; Emplish.

C The sequence is that of an antimicrobial protein which car be used to control microbial infestations in plants and macadamia to control microbial microbi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Zea mays antimicrobial pro
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Local Similarity 40.4%;
nes 202; Conservative
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Pred. No. 4.41e-85;
113; Mismatches 156;
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CC The products of the invention can be used for producing transgenic plants which have modified sucrose uptake activity, particularly in developing seeds. Enhanced sucrose uptake activity in developing seeds may be consistent of the seed (e.g. where the seed is the primary plant material harvested, for the seed (e.g. where the seed is the primary plant material harvested, convested. The SBP regulatory regions confer specific or enhanced converses in in developing seeds and so may be used to express any
                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New modified plant sucrose binding proteins - used to develop transgenic plants which can have enhanced or decreased sucrose uptake activity in developing seeds Claim 13b; Page 37-38; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chao WS, Grimes HD; WPI; 99-070155/06.
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(UNIW ) UNIV WASHINGTON STATE RES
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21-MAY-1998; U10465
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                                                                                                                                                                                                                                                                                                            Local Similarity
les 169; Consei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              max SBP2 protein
                                    HIPVSTPGKFEEFFGPGGRDPESVLSAFSWNVLQAALQTPKGKLERLFNQQNEGSIFKIS
                                                                                          HFDSEVVLFNIKGRAVLGLVRESETEKITLEPGDMIHIPAGTPLYIVNRDENEKLLLAML 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QLYEADARSFHDLAEHDVSVSFANITAGSMSAPLENTRSFKIAYVPNGKGYAEIVCPHRQ 382
                                                                                                                                                     QSDNPYYFDE-RSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLEANPNAFVLPT 305
                                                                                                                                                                         EDENPYVFEEDKDFSTRVETEGGSIRVLKKFTEKSKLLQGIENFRLAILEARAHTFVSPR 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FFPGPRQHQQQSPRSTKQQQ 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FLPGPEESGGHEEREQEEEE 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNENLLLFAFGINAQNNHENFLAGRERNVLQQIEPQAMELAFAAPRKEVEESFNSQDQSI
                                                                          HLDADAILLVIGGRGALKMIHHDNRESYNLECGDVIRIPAGTTFYLINRDNNERLHIAKF
                                                                                                                                                                                                                                QQREYEDCRRCEQQ-E-P-RQQHQCQLRCREQQRQHGRGGDMMNPQRGGSGRYEEGEEE
                                                                                                                                                                                                                                                                      EDPELVTCKHQCQQQRQYTESDKRTCLQQCDSMKQEREKQVEEETREKEEEHQ-EQHEEE 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S-GRHGGRG-G-GKR-----HE--EE-EDV-H-YEQVRARLSKREAIVVLAGHPVVFVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SQGGESERERDKGRRSEEEEEESSEEQEEAGQGYHTIRARLSPGTAFVVPAGHPFVAVAS 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QAYEVKPEDYRQLQDMDLSVFIANVTQGSMMGPFFNTRSTKVVVVASGEADVEMACPH-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sucrose binding protein; SBP2; sucrose uptake; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                         489
                                                                                                                                                                                                                                                                                                            21.6%;
larity 36.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; 489
                                                                                                                                                                                                                                                                                                                                                                                                           seeds.
                                                                                                                                                                                                                                                                                                          Score 1063; DB 1; 1
Pred. No. 7.99e-82;
137; Mismatches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FOUND
                                                                                                                                                                                                                                                                                                                                               Length 489;
                                                                                                                                                                                                                                                                                                            20;
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425
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                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                          of the seed (e.g. where the seed is the primary plant material harvested, such as soybean). In contrast, decreased sucrose uptake activity in seeds might be desirable where the vegetative material of the plant is harvested. The SBP regulatory regions confer specific or enhanced expression in developing seeds and so may be used to express any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a novel sucrose binding protein, SBP1 isolated from Glycine max. This protein is used in a method resulting in the production of a modified plant sucrose binding protein (SBP) which has a modified amino acid sequence compared to a corresponding wild-type SBP, and where expression of the modified SBP in a yeast assay system confers enhanced sucrose uptake compared to the corresponding wild-type SBP. The products of the invention can be used for producing transgenic plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-MAY-1997; US-047568.

(UNIW ) UNIV WASHINGTON STATE RES FOUND.
Chao WS, Grimes HD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         which have modified sucrose uptake activity, particularly in developing seeds. Enhanced sucrose uptake activity in developing seeds may be desirable where it is an advantage to increase the carbohydrate content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New modified plant sucrose binding
transgenic plants which can have en
uptake activity in developing seeds
Disclosure; Page 34-36; 58pp; Engli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant; seed; carbohydrate content; soybean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W90339 standard; protein; W90339;
                                                                                                                                                                                                                                                                                                                                                                       transgene in developing seeds. Sequence 524 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 99-070155/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9853086-A1.
26-NOV-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycine max.
                      227
                                                          308
                                                                                                 167
                                                                                                                                                                             107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-MAY-1998; U10465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-MAY-1999
                                                                                                                                         249
                                                                                                                                                                                                                  190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      max SBP1
PVSVSTPGKFEEFFAPGGRDPESVLSAFSWNVLQAALQTPKGKLENVFDQQNEGSIFRIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MDLSVFIANVTQGSMMGPFFNTRSTKVVVVVASGEADVEMACPHLSGRHGGRGGGKRHEEE 544
                                                                            DSEVVFFNIKGRAVLGLVSESETEKITLEPGDMIHIPAGTPLYIVNRDENDKLFLAMLHI 226
                                                                                                                                                                                                                QQREY-EDCRRRCEQQEPRQQHQCQLRCREQQRQHGRGGDMMNPQRGGSGRYEEGEEEQS 248
                                                                                                                                                                                                                                        QQQQYTEGDKRVCLQSCDRYHRMKQEREKQIQ-EETRE-KKEEEESREREEEQQEQHEEQD 106
                                                          DADAILLVIGGRGALKMIHHDNRESYNLECGDVIRIPAGTTFYLINRDNNERLHIAKF-L
                                                                                                                                       DNPYYFDE-RSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLEANPNAFVLPTHL
                                                                                                                                                           SPS-YHRISADLKPGMVFVVPPGHPFVTIASNKENLLIICFEVNVRDNK-KFTFAGKD-N 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LNLMLTFTNITQRSMSTIHYNSHATKIALVMDGRGHLQISCPHMSSR----SDSK-HDKS 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QEQIRELTRDDSESRHWHIRRGGESSRGPYNLFNKRPLYSNKYGQAYEVKPEDYRQ-LQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IVSSLDNVAKELAFNYPS-EMVNGVSERKESLFFPFELPSEERGRRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EDVHYEQVRARLSKREAIVVLAGHPVVFVSSGNENLLLFAFGINAQNNHENF-LAGRERN
                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                               20.8%;
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                                                                                                                                                                                                                                                                                         Score 1026; DB 1;
Pred. No. 1.77e-78;
120; Mismatches 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seeds
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                                                                                                                                                                                                                                                                                               135;
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                                                                                                                                                                                                                                                                                                                               Length 524;
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                                                                                                                                                                                                                                                                                             20;
                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                       307
                      286
                                                            366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PT New modified plants which can have enhanced or decreased sucrose
PT uptake activity in developing seeds
PS Claim 7; Page 36:37; 58pp; English.

CC This sequence represents a novel sucrose binding protein, SBP1 isolated
CC from Glycine max. This protein is used in a method resulting in the
CC production of a modified plant sucrose binding protein (SBP) which has a
CC modified amino acid sequence compared to a corresponding wild-type SBP,
CC and where expression of the modified BBP in a yeast assay system confers
CC enhanced sucrose uptake compared to the corresponding wild-type SBP,
CC The products of the invention can be used for producing transgenic plants
CC which have modified sucrose uptake activity, particularly in developing
CC seeds. Enhanced sucrose uptake activity in developing seeds may be
CC desirable where it is an advantage to increase the carbohydrate content
CC such as soybean). In contrast, decreased sucrose uptake activity in
CC seeds might be desirable where the vegetative material of the plant is
CC carrespond in developing seeds and so may be used to express any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-NOV-1998.
21-MAY-1998; U10465.
21-MAY-1997; US-047568.
22-MAY-1997; US-047568.
(UNIAY) UNIV WASHINGTON STATE RES FOUND.
Chao WS, Grimes HD;
WPI; 99-070155/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycine max. WO9853086-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seed; carbohydrate content;
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SBP1; sucrose binding protein; SBP2; sucrose uptake;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W9034
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W90340 standard;
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                    227
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                                                                                                                                                                                                                                                                                                                                                                                                                    49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 19.6%;
Local Similarity 38.8%;
nes 158; Conservative
                                                                                                             DSEVVFFNIKGRAVLGLVSESETEKITLEPGDMIHIPAGTPLYIVNRDENDKLFLAMLHI 226
                                                                                                                                                                                                                                                   ENPYIFEEDKDFETRVETEGGRIRVLKKFTEKSKLLQGIENFRLAILEARAHTFVSPRHF 166
                                                                                                                                                                                                                                                                                                                                                                                                                 QQQQYTEGDKRVCLQSCDRYHRMKQEREKQIQ-EETRE-KKEEEESREEEEQQEQHEEQD 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q-TISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTEKLRGVFGQQREGVIIRAS 425
PVSVSTPGKFEEFFAPGGRDPESVLSAFSWNVLQAALQTPKGKLENVFDQQNEGSIFRIS 286
                                                                              DADAILLVIGGRGALKMIHHDNRESYNLECGDVIRIPAGTTFYLINRDNNERLHIAKF-L 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DMDLSVFIANVTQGSMMGPFFNTRSTKVVVVVASGEADVEMACPHLSGRHGGRGGGKRHEE 543
                                                                                                                                                                                                                 DNPYYFDE-RSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLEANPNAFVLPTHL
                                                                                                                                                                                                                                                                                                                                                   QQREY-EDCRRRCEQQEPRQQHQCQLRCREQQRQHGRGGDMMNPQRGGSGRYEEGEEEQS 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NVLQQIEPQAMELAFAAPRKEVEESF 628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QEQIRELTRDDSESRHWHIRRGGESSRGPYNLFNKRPLYSNKYGQAYEVKPEDY-RQ-LQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 964; DB 1;
Pred. No. 6.98e-73;
109; Mismatches 123
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Best Local
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22-DEC-1997;
20-DEC-1996;
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(RETR-) COOP RES CENT TROPIC
BOWER NI, Goulter KC, Green
WPI: 98-377279/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel anti-microbial protein from e.g. Macadamia integrifolia useful for controlling microbial infestations of plants or man Claim 1; Page 63-65; 96pp; English.

The sequence is that of an antimicrobial protein which can be used to control microbial infestations in plants and mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W62838
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     IANVTQGSMMGPFFNTRSTKVVVVASGEADVEMACPHLSGRHGGRGGGKRHEEEEEDVHYE
                                                                                                                                            LSKRAKSSSRK-TI--SSED-K-PFNLRSRDPIYSNKLGKFFEITPEKNPQLRDLDIFLS
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                                                         IVDMNEGALLLPHFNSKAIVILVINEGDANIELV-G-LKEQQ--QE---QQQEEQPLEVR
                                                                                                            LT-RDDSESRHWHIRRGGESSRGPYNLFNKRPLYSNKYGOAYEVKPEDYROLODMDLSVF
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Similarity 32.7%;
193; Conservative
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Pred. No. 8.08e-70;
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CC and where expression of the modified SBP in a yeast assay system confers conhanced sucrose uptake compared to the corresponding which type SBP.

CC which have modified sucrose uptake activity in developing seeds. Enhanced sucrose uptake activity in developing seeds may be content of the seed (e.g. where the seed is the primary plant material harvestud, such as soybean). In contrast, decreased sucrose uptake activity in developing seeds might be desirable where the vegetative material of the plant is carbonic and the plant is contrasted. The SBP regulatory regions confer specific or enhanced contrasted in developing seeds and so may be used to express any content of the plant is contrast.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
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21-MAY-1998; U10465.
22-MAY-1997; US-047568
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                                                                                                                                                                                                                                                                                                                   94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              max truncated SBP2 protein.
P1; sucrose binding protein; SBP2;
ed; carbohydrate content; soybean.
EDPELVTCKHQCQQQRQYTESDKRTCLQQCDSMKQEREKQVEEETREKEEEHQ-EQHEEE 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QAMELAFAAPRKEVEESFNSQDQSIFFPGPRQHQQQSPRSTKQQQPLVSIL
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                                                        QEQIRELTRDDSESRHWHIRRGGESSRGPYNLFNKRPLYSNKYGQAYEVKPEDYRQ-LQD
                                                                         RERVRALAPIKKSSW-WPF--GGES-KAQFNIFSKRPIFSNGYGRLIEVGPDDEKSWLQR
                                                                                                                             LQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTEKLRGVFGQQREGVIIRAS
                                                                                                                                                   HIPVSTPGKFEEFFGPGGRDPESVLSAFSWNVLQAALQTPKGKLERLFNQQNEGSIFKIS
                                                                                                                                                                                                                        QSDNPYYFDE-RSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLEANPNAFVLPT 305
                                                                                                                                                                                                                                                                                                                 EDENPYVFEEDKDFSTRVETEGGSIRVLKKFTEKSKLLQGIENFRLAILEARAHTFVSPR 153
                                                                                                                                                                                                                                                                                                                                                      QQREYEDCRRCEQQ-E-P-RQQHQCQLRCREQQRQHGRGGDMMNPQRGGSGRYEEGEEE 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVRARLSKREAIVVLAGHPVVFVSSGNENLLLFAFGINAQNNHENFLAGRERNVLQQIEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 924; DB 1;
Pred. No. 2.80e-69;
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Best Local :
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23-SEP-1996; U15222.
04-MAR-1996; US-610424.
29-DEC-1995; US-009455.
(UYAR-) UNIV ARKANSAS.
Bannon GA, Burks AW, Co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This polypeptide comprises major peanut allergen Ara hI (W22149). Its sequence was deduced from cDNA clone P41b (T76613), isolated from peanut seed cDNA using a primer (see T76616) based on an isolated Ara hI peptide (see W24206). The sequence shows significant homology with the vicilin family of seed storage proteins of other legumes. The allergen is recognised by serum IgE from a large proportion of individuals with peanut hypersensitivity. Ara hI and Ara hII (see W24164) can be used to raise monoclonal antibodies which are used in a specific two-site MAD ELISA for the detection of Ara hI or Ara hII (claimed). IgE-binding Ara hI antigen epitopes (see W24165-87) may be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vaccines to protect against allergic reactions to peanut allergens, e.g. anaphylactic shock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peanut allergens Ara hI and Ara hII -
two-site monoclonal antibody based EL.
Claim 31; Page 172; 354pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            monoclonal antibody; ELISA; analysis; Ara hI. Arachis hypogaea strain Florunner.
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29-DEC-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peanut allergen Ara
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38 CAQRCLQSCQQEPDDLKQKACESRCTK-LEYDPRCVYDPRGHTGTTNQRSPPG-ERTRGR
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  ALNTQTEKLRGVF-----GQQRE-GVI---IRASQE-Q--IRELTRDD-SE-SRH-WHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QPGDYDDDERQPRREEGGR-WGPAGPRE-RERE-ED-WRQPREDWRRPSHQ-QPR-KI-- 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CQRRCKEICEEEEEYNRQRDPQQQYEQCQKHCQRRETEPR-HMQTCQQRCERRYEKEKRK 160
                                                   AFNAEFNEIRRVLLEENAGGEQEERGQRRWSTRSSENNEGVIVKVSKEHVEELTKHAKSV
                                                                                                                                                                LRIPSGFISYILNRHDNQNLRVAKISMPVTQPGQFEDFFPASSRDQSSYLQGFSRNTLEA
                                                                                                                                                                                                                         KLLRALKNYRLVLLEANPNAFVLPTHLDADAILLVIGGRGALKMIHHDNRESYNLECGDV
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                                                                                                                                                                                                                                                                                                                                      RQHGRGGDMMNPQRGGSGRYEEGEEEQSDNPYYFDERSLSTRFRTEEGHISVLENFYGRS
                                                                                                                                                                                                                                                                                                                                                                                         RPEGREGE - - - QEWGTPGSHVR - EETSRNNPFYFPSRRFSTRYGNQNGRIRVLQRFDQRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                QQKRYEEQQREDEEKYEERMKEEDNKRDPQQREYEDCRRRCEQQEPRQQHQCQLRCREQQ
                                                                                                            IRIPAGTTFYLINRDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEA
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153; M
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No. 1.20e-68;
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443

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RESULT RESULT REPORT OF THE RESULT RE
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                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 19
                                                                                                                                                                                                                                                                                                                                                                                                       two-site monoclonal antibody based ELISA

Claim 31; Page 169; 354pp; English.

CThis polypeptide comprises major peanut allergen Ara HI (W22149).

CIts sequence was deduced from cDNA clone P17 (T76612), isolated from peanut seed cDNA using a primer (see T76616) based on an isolated Ara hI peptide (see w24206). The sequence shows significant homology with the vicilin family of seed storage proteins of other legumes. The allergen is recognised by serum CIF from a large proportion of individuals with peanut the hypersensitivity. Ara hI and Ara hII (see W24164) can be used to raise monoclonal antibodies which are used in a specific two-site can be considered by the detection of Ara hI or Ara hII (claimed). Ige-to binding Ara hI antigen epitopes (see W24165-87) may be used in vaccines to protect against allergic reactions to peanut allergens,
                                                                                                                                                                                                                                                                                                                                                                                    e.g. anaphylactic shock.
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Peanut allergens Ara hI and Ara hII -
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(UYAR-) UNIV ARKANSAS.
Bannon GA, Burks AW, Cockrell G,
WPI; 97-363453/33.
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10-JUL-1997.
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W22149;
29-DEC-1997 (fir
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04-MAR-1996; US-610424.
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176 YEERMKEEDNKRDPQQREYEDCRRRCEQQEPRQQHQCQLRCREQQRQHGRGGDMMNPQRG
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                                                                                                                                                                                                                                       Local Similarity es 192; Conser
                                 EGGRWGPAEP-RE-RERE-ED-WRQPREDWRRPSHQ-QPR-KI--RPEGREGE---QEWG 153
                                                                                                                                                                QQEPDDLKQKACESRCTKLEYDPRCVYDTGATNQRHPPGERTRGRQPGDYDDDRRQPRRE 104
                                                                                                                 AFAAPRKEVEESFNSQDQSIFFPGPRQHQQQSPRSTKQQQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Mat_protein
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Pred. No. 1.37e-65;
158; Mismatches 172; Indels
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                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                       Novel anti-microbial protein from e.g. Macadamia integrifo useful for controlling microbial infestations of plants or Claim 1; Page, 55-57; 96pp; English.

The sequence is that of an antimicrobial protein which can be used to control microbial infestations in plants and man
                                                                                                                                                                                                                                                                                                                                                                                                                                            (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
WPI; 98-377279/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arachis hypogaea antimicrobial protein antimicrobial protein; infestation; cor
                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                             animals
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                                                                                                                                                                                                                                                                        Local
                                                                    TPGS-EVREETSRNNPFYFPSRRFSTRYGNQNGRIRVLQRFDQRSKQFQNLQNHRIVQIE
                                                                                                                                       EGGRWGPAEP-RE-RERE-ED-WRQPREDWRRPSHQ-QPR-KI--RPEGREGE---QEWG
               ARPNTLVLPKHADADNILVIQQGQATVTVANGNNRKSFNLDEGHALRIPSGFISYILNRH
                                                                                                                                                                                       , QRDPQQQYEQ-CQKHCQRRETEPRHMQTCQQRCERRYEKEK-R-KQQKRYEEQQREDEEK
                                                                                                                                                                                                                       QQEPDDLKQKACESRCTKLEYDPRCVYDTGATNQRHPPGERTRGRQPGDYDDDRRQPRRE 104
                                                    GSGRYEEGEEEQSDNPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLE
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Pred. No. 1.37e-65;
158; Mismatches 172;
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458 FNKRPLYSNKYGQAYEVKPED-YRQLQDMDLSVFIANVTQGSMMGPFFNTRSTKVVVVAS 516
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